

Figure 1A

1 CAAGCACTGTGCTAAAGTGTTTTTCATATGTCATGAAAAGTTGTGCCAGAAAATTATGGT 60

61 TTGAACATGGGCAGTTTTCTCCTACCGTCAGCTATATCCACAAGCATCACATGAAGTGA 120

121 GATCTGGCAGCTCTGTGTATTTTCAGTCAAGTTCCACAATGAAACCTGACAATAATGGTAA 180

181 AAACCAATACGGACATCTGAGTAACTGGGGAATTGGCCTGCCTTGCATGTGAGCTTGATG 240

241 GAAGATTGGATATAGACGAGTTGATTATATTTTATGAAGTAGCAGCTCACTACCATCCAC 300

301 CATCCAGGGTTTAAACTACTTTTTTCAGCATCACTTCACCTGTGGACTCTTATACATTTTG 360

361 ATTTCTTGGGGGAAAAATCTGGGATAAGAGGAGGTCATTTTTTAATAAGTTAGCATCCT 420

421 TTTCCTTTTCTTACAAGTTGATCCAAAGGATAAGGCTGTGACTCCAATGGATTGCACCTT 480

481 TAAATCAAATAGCAGCAGCAGAAGAAAGGGACAATGGCTCTGAGTGGAACTGTAGTCG 540

1 M A L S G N C S R 9

541 TTATTATCCTCGAGAAACAAGGGTCCGCAGTTCCCAACTCCTTCCCTGAGTGGTAGAGCT 600

10 Y Y P R E Q G S A V P N S F P E V V E L 29

601 GAATGTCGGGGTCAAGTTTATTTTACTCGCCATTCCACATTGATAAGCATCCCTCATTC 660

30 N V G G Q V Y F T R H S T L I S I P H S 49

661 CCTCCTGTGGAAAATGTTTTCCTCCAAAGAGAGACACGGCTAATGATCTAGCCAAGGACTC 720

50 L L W K M F S P K R D T A N D L A K D S 69

721 CAAGGGAAGGTTTTTCATTGACAGAGATGGATTCTTGTTCGTTATATTCTGGACTATCT 780

70 K G R F F I D R D G F L F R Y I L D Y L 89

781 CAGGGACAGGCAGGTGGTCCCTGCCTGATCACTTTCAGAAAAGGAAGACTGAAAGGGA 840

90 R D R Q V V L P D H F P E K G R L K R E 109

841 AGCTGAATACTTCCAGCTCCAGACTTGGTCAAACCTCCTGACCCCGATGAAATCAAGCA 900

110 A E Y F Q L P D L V K L L T P D E I K Q 129

901 AAGCCAGATGAATTCTGCCACAGTGACTTTGAAGATGCCTCCCAAGGAAGCGACACAAG 960

130 S P D E F C H S D F E D A S Q G S D T R 149

961 AATCTGCCCCCTTCCCTCCCTGCTCCCTGCGACCGCAAGTGGGGTTTCATTACTGTGGG 1020

150 I C P P S S L L P A D R K W G F I T V G 169

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Figure 1B

1021	TTACAGAGGATCCTGCACCTTGGGCAGAGAGGGACAGGCAGATGCCAAGTTTCGGAGAGT	1080
170	Y R G S C T L G R E G Q A D A K F R R V	189
1081	TCCCGGATTTTGGTTTGTGGAAGGATTTCTTGGCAAAAGAAGTCTTTGGAGAACTTT	1140
190	P R I L V C G R I S L A K E V F G E T L	209
1141	GAATGAAAGCAGAGACCCCTGATCGAGCCCCAGAAAGATACACCTCCAGATTATCTCAA	1200
210	N E S R D P D R A P E R Y T S R F Y L K	229
1201	ATTCAAGCACCTGGAAAGGGCTTTTGATATGTTGTACAGATGTGGATTCCACATGGTGGC	1260
230	F K H L E R A F D M L S E C G F H M V A	249
1261	CTGTAACCTCATCGGTGACAGCATCTTTCATCAACCAATATACAGATGACAAGATCTGGTC	1320
250	C N S S V T A S F I N Q Y T D D K I W S	269
1321	AAGCTACACTGAATATGTCTTCTACCGTGAGCCTTCCAGATGGTCACCCTCACACTGCGA	1380
270	S Y T E Y V F Y R E P S R W S P S H C D	289
1381	TTGTCTGTGCAAGAATGGCAAAGGTGACAAAGAAGGGGAGAGCGGCAGCTCTTGCAATGA	1440
290	C C C K N G K G D K E G E S G T S C N D	309
1441	CCTCTCCACATCTAGCTGCGACAGCCAGTCTGAGGCCAGCTCTCCCCAGGAGACGGTCAT	1500
310	L S T S S C D S Q S E A S S P Q E T V I	329
1501	CTGTGGTCCCGTGACACGCCAGACCAACATCCAGACTCTGGACCGTCCCATCAAGAAGGG	1560
330	C G P V T R Q T N I Q T L D R P I K K G	349
1561	CCCTCTCCAGCTGATCCAACAGTCAAGAGATCGCGCGGAAAAGCGACTTACTCCGGATTCT	1620
350	P V Q L I Q Q S E M R R K S D L L R I L	369
1621	GACTTCAAGGCTCCAGGGAATCGAACATGAGCAGCAAAAAAAAAAGCTGTTAAAGAAAAGCT	1680
370	T S G S R E S N M S S K K K A V K E K L	389
1681	CTCAATTGAGGAGGAGCTGGAGAAATGTATCCAGGATTTCTAAAAAATAATTCAGA	1740
390	S I E E E L E K C I Q D F L K K K I P D	409
1741	TCGGTTCTCTGAGAGAAAACATCCTTGGCAATCTGAACTTTTAAGGAAGTATCATCTATA	1800
410	R F P E R K H P W Q S E L L R K Y H L	428
1801	AGGGAGGGCTGGGGCGGGGAAAAAAAAAAGAGTCATTTTGAATTAACCTCATAA	1860
1861	AAGGAATTCATATTTTAAAGGAAAAAATACTAATAATGATGCACATTTCTTAGAACACA	1920
1921	ATAGTCCATTGATATACTACTGCCTACTTTACCTAGTTACCTTAACATGTAAATCCACA	1980

Figure 1C

1981 GGGTAGATTCTCTTCTAGATGTGGAAGTACAAGAAAATCTTTTCTAGTTATTGTTTGT 2040

2041 TACTTCGTCCTCCATGTGCTAACTATCTTATATATAATGAGAGCCAGCTACGTAAAAGTAGC 2100

2101 TGAGAGGCCTTGGGAGTCAITTTATCCCAAAGTGGGTTTTCTCTCATCTCTTACCTCC 2160

2161 CTCCTTTGAATGAGGATGTGGTAGAAAAAGATCTGGCCCAATGGCATAAGTTTGGAAATTT 2220

2221 TTAATTTTGGTTTCTCTTTTGTATGGGGTTGGGGGAATGGCAGATTATATGACTT 2280

2281 TTCCTCAAATCTATATGTGCCAGTTTATATTGACTCCGTATGCATGAGTATTGTGCAA 2340

2341 CACAAGCACAACCTAAGTATGTATATACATGACGCACACGATGCCAGGGCCCTAGACCTC 2400

2401 CCAAGGGCTGTGCTCCTGCTCCAGCAGCCCTCTCTTAGAATATTTCAGATGGATGAGCT 2460

2461 TCTGACTCTTCTTAAATTTCTTTTGGGAAGATTCCCAGCCTTCTTTCACAACACTTTC 2520

2521 TAACATCAAATGACTCTCATCATCAACAAATTGTATTCCTTATTGTGAAATTAATAACCT 2580

2581 CAGGCTCCATTTTACTGCTTTGCTCTTTGCTCTGCATTAAGAGAGGATGAGGAGAGCTGGT 2640

2641 CAAACATTCTTGTGTAAAAAATCAAACATTATATCCACAAAATTTCTTGCTAAATG 2700

2701 ACTCCACACTCAGCCTTCTCTACCCCTGAAGTGAATATCACCCTTTTCTCCATGTTTCA 2760

2761 GAGTTCCTTACTGCCACAGTTTAATGGTGTGGCCTTCCACATAATCCACATTAAGTCT 2820

2821 GTGTTCCTGTGTGTGTGGAACTAAGGACAACACAGTACTTGAATAAGGGTCCGGCC 2880

2881 TTTTGTGTGTTTAGAGAAAGTTGTATTCCACACACAACCTAATAATTCTTATAAAAAAT 2940

2941 TTTAAACTACAAAGCTACATTTTACTTGCTTGTAGCCGTTTTTGTGTGCCTTTGGGATT 3000

3001 CGGGCTTTGGCTGTGCCCATGCTAGGATTTAGCTGTGTCAATTTTATGATGCTGTAACA 3060

3061 ACCCAACAAGGTAAGTGAAGCTCCAGAGTTAAGGTTTCAGATTCTAAATGAAACTATCT 3120

3121 TTTTCAATTACATCCTGACTTGTATAGACACAGCCAAAAAGAACTGTTAATAGCCATCC 3180

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Figure 1D

3181 GTCCATGTAACCTCTGTATTTTACTAAGGTACCAATAGCTCTTTCATAGACTTGTGCTACA 3240  
3241 AGAAGGTAAAAGACCAGTTTATTTCAGCATTCCTCATGCATTCAGTGGTAACCAA 3300  
3301 AAATAATTTGTCAATTAATAGTTGTGTGCCAAGCACTCCTAATTGTTTTATTGCGTGTG 3360  
3361 TGTGCATGTGTATGTGTATCAGGTAATAAAGGCAATTGGATGATTAAAAAAAAA 3420  
3421 AA 3468

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Figure 2A

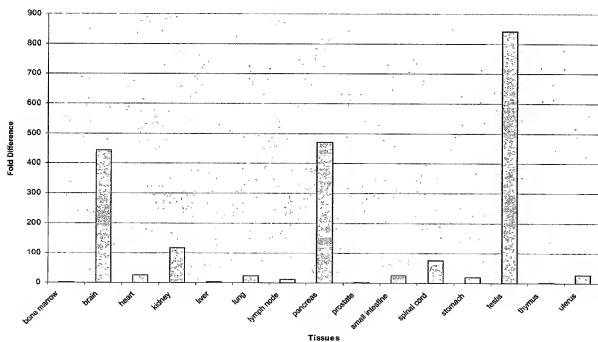
1		50
K+betaM2	(1)	-----MALSGNCSRYYPREGQSAVPNSFPHVVELNVGGQVYPTREHSTLIS
AAF558201	(1)	-----MPETTELNVGGVSVITTLATLTLQ
CAA20329.1	(1)	-----MTSPEVYITLNVGGTIVYITRSLPSK
Y34129	(1)	-----MDNGDWGYMTDIPVTLNVGGHMTTSLTPTK
Y34125	(1)	MSRPLITRSPASPLXNQGIPTPAQLTKSNAPVHLLVGGHMTTSLTPTK
	51	100
K+betaM2	(46)	IPHSLLWKMFSP--KRDITANDLAKDSKGRFEDRDGFLRYVILDELDRQ
AAF558201	(24)	DKSTLLAEFLG-----GGRDSLAKDSKGRYEDRDGFLRYVILDELDRKA
CAA20329.1	(27)	ETPTLLANLASGSLSEDEQANVYILPDGTLFDRDGPLERAYVILHFLPTDK
Y34129	(33)	YPSMLGAFGG-----D--FPDARDPCGNYEDRDGPLERYVILNPTTSE
Y34125	(51)	YPSRLGRIFDG-----T-EPITVLSLKQHYEDRDGQMERVILNPTTSTK
	101	150
K+betaM2	(94)	IVLPDHPPEKGRLEKAEVYFOLPDVKKLLTPDEIKQSPDEFCHSDSFEDAS
AAF558201	(69)	LHLDPGFERQRLEKAEHFKLTAHBCRSEKAR
CAA20329.1	(77)	LSLPDGFREVARLEKAEVYSLERSTLLSNAGSIS-PRPR-----
Y34129	(77)	LTLLDLEDFDLKAEADPYQIEPTQCLNDPKPLY-----
Y34125	(96)	LLLPDDEKYTLVYEAQYFOLQPKLEMERWQDR-----
	151	200
K+betaM2	(144)	QGSOTRICPPSSLLPARDKRWGITVGYRGCITLGEFGQADVKFRIVPRL
AAF558201	(105)	-----PP-----GCITVGYRGSFQFGNGLADVKFRISRL
CAA20329.1	(117)	-----TANGYNTITSAETGGYITLGYRGTFAGFNGQADVKFRACHRL
Y34129	(113)	-----PMDTFEEVVELSTRKLSKYSNPVAVITQLITTTK
Y34125	(132)	-----ETGRFSRPCBCLVVRVAPDLGERITLGGKSLLEVE
	201	250
K+betaM2	(194)	VCGRISLAKEVFSETLNESRDPPDR-APRYTTSRFYLLKPKILERAFLMLSE
AAF558201	(137)	VCGRVAQCEVVFSETLNESRDPPDHGGTIRYTSRFLLKPKILEQAFNLHD
CAA20329.1	(162)	VCGRATLCREVFADTLNESRDPPG--PDGGE
Y34129	(149)	VHSLLEGISNYFTRWKTHMMDRD--COVSEFTFGPCDYHDEVSLVHLM
Y34125	(169)	PEIGDVMCNVFNAGWNHSTTVIR-----PPLNGYCHLSVQMLERLQ
	251	300
K+betaM2	(243)	CGPHVVCNSSVTASFIN-----QYTDKIIWSSYTYEVFYRPSRWSPSH
AAF558201	(187)	HGYSNAGSCSGTAGSAAEPKPGVDTEENRWNHYNFVFIRI-----
CAA20329.1	(191)	-----
Y34129	(196)	EYITKQGFTIRNTRVHMSERANENTVHNWTFCLRLARKTD-----
Y34125	(213)	RGEEIVGSCGGVDSQFSYVLRRELRTPRVPSVIRIKQPL-----
	301	350
K+betaM2	(288)	CDCCCKNGKGDKEGSGTSCNDLSTSSCDSQSEASSPQETVICGFVTRQT
AAF558201	(229)	-----
CAA20329.1	(191)	-----
Y34129	(238)	-----
Y34125	(257)	-----
	351	400
K+betaM2	(338)	NIQTLDRPIKGFVQLIQQSEMRRKSDLLRLTSGSRESNMSSKKKAVKE
AAF558201	(229)	-----
CAA20329.1	(191)	-----
Y34129	(238)	-----
Y34125	(257)	-----

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Figure 2B

	401	441
K+betaM2	(388)	KLSIEEELEKCIQDFLKKKIPDRFPERKHPWQSELLRKYHL
AAF558201	(229)	-----
CAA20329.1	(191)	-----
Y34129	(238)	-----
Y34125	(257)	-----
Consensus	(401)	-----

Figure 3



**Figure 4.**

<b>Protein</b>	<b>Genbank ID</b>	<b>Identities</b>	<b>Similarities</b>
Human potassium channel K+Hnov28	gi Y34129	31%	41%
Drosophila CG10830 protein	gi AAF55820.1	52%	66%
Caenorhabditis K+ channel tetramerisation domain	gi CAA20329.1	42%	51%
Human potassium channel K+Hnov27	gi Y34125	32%	41%

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